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RAW SEQUENCE LISTING

DATE: 09/21/2001

PATENT APPLICATION: US/09/944,849

TIME: 18:10:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\09212001\I944849.raw

#2

P.5

3 <110> APPLICANT: Nickoloff, Brian
 4 Miele, Lucio
 6 <120> TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND
 TREATMENT OF
 7 MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATHWAY
 9 <130> FILE REFERENCE: 212583
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/944,849
 12 <141> CURRENT FILING DATE: 2001-08-31
 14 <150> PRIOR APPLICATION NUMBER: US 60/229,614
 15 <151> PRIOR FILING DATE: 2000-08-31
 17 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 7332
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence
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 27 <223> OTHER INFORMATION: Constitutively Active Notch-1
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(7332)
 32 <223> OTHER INFORMATION:
 35 <220> FEATURE:
 36 <221> NAME/KEY: misc_feature
 37 <222> LOCATION: (5288)..(5288)
 38 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
 41 <220> FEATURE:
 42 <221> NAME/KEY: misc_feature
 43 <222> LOCATION: (5359)..(5359)
 44 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
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 49 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
 50 1 5 10 15
 52 ctc gcc gca cga ggc ccg cga tgc tcc cag ccc ggt gag acc tgc ctg 96
 53 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
 54 20 25 30
 56 aat ggc ggg aag tgt gaa gcg gcc aat ggc acg gag gcc tgc gtc tgt 144
 57 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
 58 35 40 45
 60 ggc ggg gcc ttc gtg ggc ccg cga tgc cag gac ccc aac ccg tgc ctc 192
 61 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
 62 50 55 60
 64 agc acc ccc tgc aag aac gcc ggg aca tgc cac gtg gtg gac cgc aga 240
 65 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
 66 65 70 75 80
 68 ggc gtg gca gac tat gcc tgc agc tgt gcc ctg ggc ttc tct ggg ccc 288
 69 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro

ENTERED

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70	85	90	95	
72	ctc tgc ctg aca ccc ctg gac aac gcc tgc ctc acc aac ccc tgc cgc	336		
73	Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg			
74	100 105 110			
76	aac ggg ggc acc tgc gac ctg ctc acg ctg acg gag tac aag tgc cgc	384		
77	Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg			
78	115 120 125			
80	tgc ccg ccc ggc tgg tca ggg aaa tcg tgc cag cag gct gac ccg tgc	432		
81	Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys			
82	130 135 140			
84	gcc tcc aac ccc tgc gcc aac ggt ggc cag tgc ctg ccc ttc gag gcc	480		
85	Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala			
86	145 150 155 160			
88	tcc tac atc tgc cac tgc cca ccc agc ttc cat ggc ccc acc tgc cgg	528		
89	Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg			
90	165 170 175			
92	cag gat gtc aac gag tgt ggc cag aag ccc agg ctt tgc cgc cac gga	576		
93	Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly			
94	180 185 190			
96	ggc acc tgc cac aac gag gtc ggc tcc tac cgc tgc gtc tgc cgc gcc	624		
97	Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala			
98	195 200 205			
100	acc cac act ggc ccc aac tgc gag cgg ccc tac gtg ccc tgc agc ccc	672		
101	Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro			
102	210 215 220			
104	tcg ccc tgc cag aac ggg ggc acc tgc cgc ccc acg ggc gac gtc acc	720		
105	Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr			
106	225 230 235 240			
108	cac gag tgt gcc tgc ctg cca ggc ttc acc ggc cag aac tgt gag gaa	768		
109	His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu			
110	245 250 255			
112	aat atc gac gat tgt cca gga aac aac tgc aag aac ggg ggt gcc tgt	816		
113	Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys			
114	260 265 270			
116	gtg gac ggc gtg aac acc tac aac tgc ccg tgc ccg cca gag tgg aca	864		
117	Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr			
118	275 280 285			
120	ggt cag tac tgt acc gag gat gtg gac gag tgc cag ctg atg cca aat	912		
121	Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn			
122	290 295 300			
124	gcc tgc cag aac ggc ggg acc tgc cac aac acc cac ggt ggc tac aac	960		
125	Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn			
126	305 310 315 320			
128	tgc gtg tgt gtc aac ggc tgg act ggt gag gac tgc agc gag aac att	1008		
129	Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile			
130	325 330 335			
132	gat gac tgt gcc agc gcc gcc tgc ttc cac ggc gcc acc tgc cat gac	1056		
133	Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp			
134	340 345 350			

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136 cgt gtg gcc tcc ttt tac tgc gag tgt ccc cat ggc cgc aca ggt ctg      1104
137 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
138          355          360          365
140 ctg tgc cac ctc aac gac gca tgc atc agc aac ccc tgt aac gag ggc      1152
141 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
142      370          375          380
144 tcc aac tgc gac acc aac cct gtc aat ggc aag gcc atc tgc acc tgc      1200
145 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
146 385          390          395          400
148 ccc tcg ggg tac acg ggc ccg gcc tgc agc cag gac gtg gat gag tgc      1248
149 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
150          405          410          415
152 tcg ctg ggt gcc aac ccc tgc gag cat gcg ggc aag tgc atc aac acg      1296
153 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
154          420          425          430
156 ctg ggc tcc ttc gag tgc cag tgt ctg cag ggc tac acg ggc ccc cga      1344
157 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
158      435          440          445
160 tgc gag atc gac gtc aac gag tgc gtc tcg aac ccg tgc cag aac gac      1392
161 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
162      450          455          460
164 gcc acc tgc ctg gac cag att ggg gag ttc cag tgc atg tgc atg ccc      1440
165 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
166 465          470          475          480
168 ggc tac gag ggt gtg cac tgc gag gtc aac aca gac gag tgt gcc agc      1488
169 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
170          485          490          495
172 agc ccc tgc ctg cac aat ggc cgc tgc ctg gac aag atc aat gag ttc      1536
173 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
174          500          505          510
176 cag tgc gag tgc ccc acg ggc ttc act ggg cat ctg tgc cag tac gat      1584
177 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
178      515          520          525
180 gtg gac gag tgt gcc agc acc ccc tgc aag aat ggt gcc aag tgc ctg      1632
181 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu
182      530          535          540
184 gac gga ccc aac act tac acc tgt gtg tgc acg gaa ggg tac acg ggg      1680
185 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
186 545          550          555          560
188 acg cac tgc gag gtg gac atc gat gag tgc gac ccc gac ccc tgc cac      1728
189 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
190          565          570          575
192 tac ggc tcc tgc aag gac ggc gtc gcc acc ttc acc tgc ctc tgc cgc      1776
193 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
194          580          585          590
196 cca ggc tac acg ggc cac cac tgc gag acc aac atc aac gag tgc tcc      1824
197 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
198      595          600          605
200 agc cag ccc tgc cgc cta cgg ggc acc tgc cag gac ccg gac aac gcc      1872

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201 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala
202      610      615      620
204 tac ctc tgc ttc tgc ctg aag ggg acc aca gga ccc aac tgc gag atc      1920
205 Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile
206 625      630      635      640
208 aac ctg gat gac tgt gcc agc agc ccc tgc gac tcg ggc acc tgt ctg      1968
209 Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu
210      645      650      655
212 gac aag atc gat ggc tac gag tgt gcc tgt gag ccg ggc tac aca ggg      2016
213 Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly
214      660      665      670
216 agc atg tgt aac agc aac atc gat gag tgt gcg ggc aac ccc tgc cac      2064
217 Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His
218      675      680      685
220 aac ggg ggc acc tgc gag gac ggc atc aat ggc ttc acc tgc cgc tgc      2112
221 Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys
222      690      695      700
224 ccc gag ggc tac cac gac ccc acc tgc ctg tct gag gtc aat gag tgc      2160
225 Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys
226 705      710      715      720
228 aac agc aac ccc tgc gtc cac ggg gcc tgc cgg gac agc ctc aac ggg      2208
229 Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly
230      725      730      735
232 tac aag tgc gac tgt gac cct ggg tgg agt ggg acc aac tgt gac atc      2256
233 Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile
234      740      745      750
236 aac aac aac gag tgt gaa tcc aac cct tgt gtc aac ggc ggc acc tgc      2304
237 Asn Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys
238      755      760      765
240 aaa gac atg acc agt ggc atc gtg tgc acc tgc cgg gag ggc ttc agc      2352
241 Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser
242      770      775      780
244 ggt ccc aac tgc cag acc aac atc aac gag tgt gcg tcc aac cca tgt      2400
245 Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys
246 785      790      795      800
248 ctg aac aag ggc acg tgt att gac gac gtt gcc ggg tac aag tgc aac      2448
249 Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn
250      805      810      815
252 tgc ctg ctg ccc tac aca ggt gcc acg tgt gag gtg gtg ctg gcc ccg      2496
253 Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro
254      820      825      830
256 tgt gcc ccc agc ccc tgc aga aac ggc ggg gag tgc agg caa tcc gag      2544
257 Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu
258      835      840      845
260 gac tat gag agc ttc tcc tgt gtc tgc ccc acg gct ggg gcc aaa ggg      2592
261 Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly
262      850      855      860
264 cag acc tgt gag gtc gac atc aac gag tgc gtt ctg agc ccg tgc cgg      2640
265 Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg

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266 865      870      875      880
268 cac ggc gca tcc tgc cag aac acc cac ggc gss tac cgc tgc cac tgc      2688
W--> 269 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys
270      885      890      895
272 cag gcc ggc tac agt ggg cgc aac tgc gag acc gac atc gac gac tgc      2736
273 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys
274      900      905      910
276 cgg ccc aac ccg tgt cac aac ggg ggc tcc tgc aca gac ggc atc aac      2784
277 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn
278      915      920      925
280 acg gcc ttc tgc gac tgc ctg ccc ggc ttc cgg ggc act ttc tgt gag      2832
281 Thr Ala Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu
282      930      935      940
284 gag gac atc aac gag tgt gcc agt gac ccc tgc cgc aac ggg gcc aac      2880
285 Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn
286      945      950      955      960
288 tgc acg gac tgc gtg gac agc tac acg tgc acc tgc ccc gca ggc ttc      2928
289 Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe
290      965      970      975
292 agc ggg atc cac tgt gag aac aac acg cct gac tgc aca gag agc tcc      2976
293 Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser
294      980      985      990
296 tgc ttc aac ggt ggc acc tgc gtg gac ggc atc aac tgc ttc acc tgc      3024
297 Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys
298      995      1000      1005
300 ctg tgt cca ccc ggc ttc acg ggc agc tac tgc cag cac gta gtc      3069
301 Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val
302      1010      1015      1020
304 aat gag tgc gac tca cga ccc tgc ctg cta ggc ggc acc tgt cag      3114
305 Asn Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln
306      1025      1030      1035
308 gac ggt cgc ggt ctc cac agg tgc acc tgc ccc cag ggc tac act      3159
309 Asp Gly Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr
310      1040      1045      1050
312 ggc ccc aac tgc cag aac ctt gtg cac tgg tgt gac tcc tgc ccc      3204
313 Gly Pro Asn Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro
314      1055      1060      1065
316 tgc aag aac ggc ggc aaa tgc tgg cag acc cac acc cag tac cgc      3249
317 Cys Lys Asn Gly Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg
318      1070      1075      1080
320 tgc gag tgc ccc agc ggc tgg acc ggc ctt tac tgc gac gtg ccc      3294
321 Cys Glu Cys Pro Ser Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro
322      1085      1090      1095
324 agc gtg tcc tgt gag gtg gct gcg cag cga caa ggt gtt gac gtt      3339
325 Ser Val Ser Cys Glu Val Ala Ala Gln Arg Gln Gly Val Asp Val
326      1100      1105      1110
328 gcc cgc ctg tgc cag cat gga ggg ctc tgt gtg gac gcg ggc aac      3384
329 Ala Arg Leu Cys Gln His Gly Gly Leu Cys Val Asp Ala Gly Asn
330      1115      1120      1125

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\ES.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:2598 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:2618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:2638 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:2658 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:2678 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:2692 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:2740 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:2743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:2749 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:2755 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:2789 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:2826 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:2829 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18